

# 2  
O/P E  
02 D O

Serial Number: 09/522 753

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: *Seq 6 deleted \*5*

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

Input Set: I522753.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

1 <110> APPLICANT: Evans, Ronald M.  
2 Chen, J. Don  
3 <120> TITLE OF INVENTION: A FAMILY OF TRANSCRIPTIONAL  
4 CO-REPRESSORS THAT INTERACT WITH NUCLEAR HORMONE RECEPTORS  
5 AND USES THEREFOR  
6 <130> FILE REFERENCE: SALK1510-3  
7 <140> CURRENT APPLICATION NUMBER: US/09/522,753  
8 <141> CURRENT FILING DATE: 2000-03-10  
9 <150> EARLIER APPLICATION NUMBER: 09/337,384  
10 <151> EARLIER FILING DATE: 1999-06-21  
11 <150> EARLIER APPLICATION NUMBER: 08/522,726  
12 <151> EARLIER FILING DATE: 1995-09-01  
13 <160> NUMBER OF SEQ ID NOS: 11  
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
15 <210> SEQ ID NO 1  
16 <211> LENGTH: 1495  
17 <212> TYPE: PRT  
18 <213> ORGANISM: Homo sapiens  
19 <400> SEQUENCE: 1  
20 Met Glu Ala Trp Asp Ala His Pro Asp Lys Glu Ala Phe Ala Ala Glu  
21 1 5 10 15  
22 Ala Gln Lys Leu Pro Gly Asp Pro Pro Cys Trp Thr Ser Gly Leu Pro  
23 20 25 30  
24 Phe Pro Val Pro Pro Arg Glu Val Ile Lys Ala Ser Pro His Ala Pro  
25 35 40 45  
26 Asp Pro Ser Ala Phe Ser Tyr Ala Pro Pro Gly His Pro Leu Pro Leu  
27 50 55 60  
28 Gly Leu His Asp Thr Ala Arg Pro Val Leu Pro Arg Pro Pro Thr Ile  
29 65 70 75 80  
30 Ser Asn Pro Pro Pro Leu Ile Ser Ser Ala Lys His Pro Ser Val Leu  
31 85 90 95  
32 Glu Arg Gln Ile Gly Ala Ile Ser Gln Gly Met Ser Val Gln Leu His  
33 100 105 110  
34 Val Pro Tyr Ser Glu His Ala Lys Ala Pro Val Gly Pro Val Thr Met  
35 115 120 125  
36 Gly Leu Pro Leu Pro Met Asp Pro Lys Lys Leu Ala Pro Phe Ser Gly  
37 130 135 140  
38 Val Lys Gln Glu Gln Leu Ser Pro Arg Gly Gln Ala Gly Pro Pro Glu  
39 145 150 155 160  
40 Ser Leu Gly Val Pro Thr Ala Gln Glu Ala Ser Val Leu Arg Gly Thr  
41 165 170 175  
42 Ala Leu Gly Ser Val Pro Gly Gly Ser Ile Thr Lys Gly Ile Pro Ser  
43 180 185 190  
44 Thr Arg Val Pro Ser Asp Ser Ala Ile Thr Tyr Arg Gly Ser Ile Thr

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/09/522,753**

 DATE: 03/29/2000  
 TIME: 17:56:12

Input Set: I522753.RAW

45		195		200		205		
46	His Gly Thr Pro Ala Asp Val Leu Tyr Lys Gly Thr Ile Thr Arg Ile							
47	210		215		220			
48	Ile Gly Glu Asp Ser Pro Ser Arg Leu Asp Arg Gly Arg Glu Asp Ser							
49	225		230		235			240
50	Leu Pro Lys Gly His Val Ile Tyr Glu Gly Lys Lys Gly His Val Leu							
51		245		250				255
52	Ser Tyr Glu Gly Gly Met Ser Val Thr Gln Cys Ser Lys Glu Asp Gly							
53		260		265				270
54	Arg Ser Ser Ser Gly Pro Pro His Glu Thr Ala Ala Pro Lys Arg Thr							
55		275		280				285
56	Tyr Asp Met Met Glu Gly Arg Val Gly Arg Ala Ile Ser Ser Ala Ser							
57		290		295				300
58	Ile Glu Gly Leu Met Gly Arg Ala Ile Pro Pro Glu Arg His Ser Pro							
59	305		310		315			320
60	His His Leu Lys Glu Gln His His Ile Arg Gly Ser Ile Thr Gln Gly							
61		325		330				335
62	Ile Pro Arg Ser Tyr Val Glu Ala Gln Glu Asp Tyr Leu Arg Arg Glu							
63		340		345				350
64	Ala Lys Leu Leu Lys Arg Glu Gly Thr Pro Pro Pro Pro Pro Pro Ser							
65		355		360				365
66	Arg Asp Leu Thr Glu Ala Tyr Lys Thr Gln Ala Leu Gly Pro Leu Lys							
67		370		375				380
68	Leu Lys Pro Ala His Glu Gly Leu Val Ala Thr Val Lys Glu Ala Gly							
69	385		390		395			400
70	Arg Ser Ile His Glu Ile Pro Arg Glu Glu Leu Arg His Thr Pro Glu							
71		405		410				415
72	Leu Pro Leu Ala Pro Arg Pro Leu Lys Glu Gly Ser Ile Thr Gln Gly							
73		420		425				430
74	Thr Pro Leu Lys Tyr Asp Thr Gly Ala Ser Thr Thr Gly Ser Lys Lys							
75		435		440				445
76	His Asp Val Arg Ser Leu Ile Gly Ser Pro Gly Arg Thr Phe Pro Pro							
77		450		455				460
78	Val His Pro Leu Asp Val Met Ala Asp Ala Arg Ala Leu Glu Arg Ala							
79	465		470		475			480
80	Cys Tyr Glu Glu Ser Leu Lys Ser Arg Pro Gly Thr Ala Ser Ser Ser							
81		485		490				495
82	Gly Gly Ser Ile Ala Arg Gly Ala Pro Val Ile Val Pro Glu Leu Gly							
83		500		505				510
84	Lys Pro Arg Gln Ser Pro Leu Thr Tyr Glu Asp His Gly Ala Pro Phe							
85		515		520				525
86	Ala Gly His Leu Pro Arg Gly Ser Pro Val Thr Met Arg Glu Pro Thr							
87		530		535				540
88	Pro Arg Leu Gln Glu Gly Ser Leu Ser Ser Ser Lys Ala Ser Gln Asp							
89	545		550		555			560
90	Arg Lys Leu Thr Ser Thr Pro Arg Glu Ile Ala Lys Ser Pro His Ser							
91		565		570				575
92	Thr Val Pro Glu His His Pro His Pro Ile Ser Pro Tyr Glu His Leu							
93		580		585				590
94	Leu Arg Gly Val Ser Gly Val Asp Leu Tyr Arg Ser His Ile Pro Leu							

**RAW SEQUENCE LISTING**  
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95		595		600		605		
96	Ala	Phe	Asp	Pro	Thr	Ser	Ile	Pro
97		610				615		620
98	Ala	Ala	Tyr	Tyr	Leu	Pro	Arg	His
99		625				630		635
100	His	Leu	Tyr	Pro	Pro	Tyr	Leu	Ile
101						645		650
102	Leu	Glu	Asn	Arg	Gln	Thr	Ile	Ile
103						660		665
104	Met	His	His	Asn	Thr	Ala	Thr	Ala
105						675		680
106	Arg	Gly	Leu	Ser	Pro	Arg	Glu	Ser
107						690		695
108	Gly	Pro	Arg	Gly	Ile	Ile	Asp	Leu
109						705		710
110	Leu	Val	Pro	Pro	Thr	Pro	Gly	Thr
111						725		730
112	Ala	Tyr	Leu	Pro	Thr	Ala	Pro	Gln
113						740		745
114	Ser	Pro	Leu	Ser	Pro	Gly	Gly	Pro
115						755		760
116	Thr	Ser	Ser	Ser	Glu	Arg	Glu	Arg
117						770		775
118	Asp	Arg	Glu	Arg	Glu	Lys	Ser	Ile
119						785		790
120	His	Ala	Pro	Ile	Trp	Arg	Pro	Gly
121						805		810
122	Gly	Ser	Ser	Gly	Gly	Gly	Gly	Gly
123						820		825
124	Ser	His	Ala	His	Gln	His	Ser	Pro
125						835		840
126	Leu	Gln	Gln	Arg	Pro	Ser	Val	Leu
127						850		855
128	Ile	Thr	Ala	Val	Glu	Pro	Ser	Lys
129						865		870
130	Thr	Ser	Ser	Pro	Val	Arg	Pro	Ala
131						885		890
132	Cys	Pro	Leu	Gly	Gly	Thr	Leu	Asp
133						900		905
134	Pro	Val	Leu	Leu	Pro	Lys	Glu	Ala
135						915		920
136	Pro	Arg	Ala	Asp	Thr	Gly	His	Ala
137						930		935
138	Ser	Gly	Leu	Glu	Pro	Ala	Ser	Ser
139						945		950
140	Pro	Leu	Val	Pro	Pro	Val	Ser	Gly
141						965		970
142	Ala	Lys	Asn	Leu	Ala	Pro	His	His
143						980		985
144	Pro	Ala	Ser	Ala	Ser	Asp	Pro	His

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/09/522,753**

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145		995		1000		1005	
146	Phe	Ser	Ile	Gln	Glu	Leu	Glu
147		1010		1015		1020	
148	Ser	Tyr	Ser	Pro	Glu	Gly	Val
149		1025		1030		1035	
150	Ser	Leu	Thr	His	Asp	Lys	Gly
151			1045			1050	
152	Lys	Ser	His	Leu	Glu	Gly	Glu
153			1060			1065	
154	Lys	Leu	Gly	Gly	Glu	Ala	Ala
155			1075			1080	
156	Glu	Ser	Gln	Pro	Ser	Ser	Ser
157			1090			1095	
158	Lys	Gly	His	Gln	Arg	Val	Val
159			1105			1110	
160	Ile	Thr	Gln	Asp	Tyr	Thr	Arg
161				1125			1130
162	Leu	Pro	Ala	Pro	Leu	Tyr	Ser
163				1140			1145
164	Asp	Leu	Arg	Arg	Pro	Pro	Ser
165				1155			1160
166	Gly	Ala	Pro	Ala	Arg	Gly	Ser
167				1170			1175
168	Pro	Glu	Pro	Asn	Lys	Thr	Ser
169				1185			1190
170	Glu	Pro	Val	Ser	Pro	Pro	Glu
171				1205			1210
172	Ser	Ala	Val	Tyr	Pro	Leu	Leu
173				1220			1225
174	Ser	Arg	Met	Gly	Ser	Lys	Ser
175				1235			1240
176	Phe	Phe	Ser	Lys	Leu	Thr	Glu
177				1250			1255
178	Lys	Gln	Glu	Ile	Asn	Lys	Lys
179				1265			1270
180	Glu	Tyr	Asn	Ile	Ser	Gln	Pro
181				1285			1290
182	Ile	Thr	Gly	Thr	Gly	Leu	Met
183				1300			1305
184	His	Ala	Ser	Thr	Asn	Met	Gly
185				1315			1320
186	Met	Gly	Lys	Tyr	Asp	Gln	Trp
187				1330			1335
188	Ala	Phe	Asn	Pro	Leu	Asn	Ala
189				1345			1350
190	Ile	Thr	Ala	Ala	Asp	Gly	Arg
191				1365			1370
192	Gly	Gly	Gly	Lys	Ala	Lys	Val
193				1380			1385
194	Lys	Ser	Pro	Ala	Pro	Gly	Leu

Input Set: I522753.RAW

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195          1395          1400          1405
196 Ser Ser Val His Ser Glu Gly Asp Cys Asn Arg Arg Thr Pro Leu Thr
197          1410          1415          1420
198 Asn Arg Val Trp Glu Asp Arg Pro Ser Ser Ala Gly Ser Thr Pro Phe
199          1425          1430          1435          1440
200 Pro Tyr Asn Pro Leu Ile Met Arg Leu Gln Ala Gly Tyr Met Ala Ser
201          1445          1450          1455
202 Pro Pro Pro Pro Gly Leu Pro Ala Gly Ser Gly Pro Leu Ala Gly Pro
203          1460          1465          1470
204 His His Ala Trp Asp Glu Glu Pro Lys Pro Leu Leu Cys Ser Gln Tyr
205          1475          1480          1485
206 Glu Thr Leu Ser Asp Ser Glu
207          1490          1495
208 <210> SEQ ID NO 2
209 <211> LENGTH: 46
210 <212> TYPE: PRT
211 <213> ORGANISM: Homo sapiens
212 <400> SEQUENCE: 2
213 Gly Lys Tyr Asp Gln Trp Glu Glu Ser Pro Pro Leu Ser Ala Asn Ala
214 1 5 10 15
215 Phe Asn Pro Leu Asn Ala Ser Ala Ser Leu Pro Ala Ala Met Pro Ile
216 20 25 30
217 Thr Ala Ala Asp Gly Arg Ser Asp His Thr Leu Thr Ser Pro
218 35 40 45
219 <210> SEQ ID NO 3
220 <211> LENGTH: 17
221 <212> TYPE: DNA
222 <213> ORGANISM: Homo sapiens
223 <400> SEQUENCE: 3
224 cggaggactg tcctccg 17
225 <210> SEQ ID NO 4
226 <211> LENGTH: 8561
227 <212> TYPE: DNA
228 <213> ORGANISM: Homo sapiens
229 <220> FEATURE:
230 <221> NAME/KEY: CDS
231 <222> LOCATION: (2)...(7555)
232 <400> SEQUENCE: 4
233 c atg tcg ggc tcc aca cag ctt gtg gca cag acg tgg agg gcc act gag 49
234 Met Ser Gly Ser Thr Gln Leu Val Ala Gln Thr Trp Arg Ala Thr Glu
235 1 5 10 15
236 ccc cgc tac ccg ccc cac agc ctt tcc tac cca gtg cag atc gcc cgg 97
237 Pro Arg Tyr Pro Pro His Ser Leu Ser Tyr Pro Val Gln Ile Ala Arg
238 20 25 30
239 acg cac acg gac gtc ggg ctc ctg gag tac cag cac cac tcc cgc gac 145
240 Thr His Thr Asp Val Gly Leu Leu Glu Tyr Gln His His Ser Arg Asp
241 35 40 45
242 tat gcc tcc cac ctg tcg ccg ggc tcc atc atc cag ccc cag cgg cgg 193
243 Tyr Ala Ser His Leu Ser Pro Gly Ser Ile Ile Gln Pro Gln Arg Arg
244 50 55 60

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I522753.RAW

Line	? Error/Warning	Original Text
705	W Line data has been corrected	Leu Ser Asp Ser Glu *
1057	W "N" or "Xaa" used: Feature required	taattttcca gggggtacct acaccaaga catatggt
1533	W "N" or "Xaa" used: Feature required	tgcgcggtcca tccgtncgtc gtncactcat ctgtccat
1535	W "N" or "Xaa" used: Feature required	gggattgttt accttgggtc tcganaaggg ggagtgga
1536	W "N" or "Xaa" used: Feature required	ggccangagg gggggggaca ancaattcgt gtgtcaag
2290	W Line data has been corrected	Pro Leu Leu Cys Ser Gln Tyr Glu Thr Leu S
2294	W "N" or "Xaa" used: Feature required	tccgtncgtc gtncactcat ctgtccatcc agagctgg
2296	W "N" or "Xaa" used: Feature required	accttgggtc tcganaaggg ggagtggaca ggaagggg
2297	W "N" or "Xaa" used: Feature required	gggggggaca ancaattcgt gtgtcaagtc gcactcnt
3054	W Line data has been corrected	Glu Thr Leu Ser Asp Ser Asp Asp *

Input Set: I522753.RAW

## PREVIOUSLY ERRORED SEQUENCES-EDITED

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```

1  <210> 6
2  <211> 8388
3  <212> DNA
4  <213> Mus musculus
5  <220>
6  <221> CDS
7  <222> (626)...(8047)
8  <221> misc_feature
9  <222> (1)...(8388)
10 <223> n = A,T,C or G
11 <400> 6
12      cttaaaaaaa aaacccttac ttgtggttaa aggaaaagaa ataaagactt aggaaaaatg      60
13      taattttcca gggggtacct acacccaaga catatggttc tcaagaggna ctcagcatat      120
14      cactttgatt ccagagaagc tacaaaagtc attaccaaac tccaggctgg aaagcagtgc      180
15      tcatactaaa tatttaaaaca tttaaagacc tgattaagag acatcaaagg ctttatacca      240
16      ggggcacacc aacagagaca ggctttttca aggataattt atgtctgccc attgtcttct      300
17      ggcttaggag acatagaggg aaacatcacc taggaaaacc agtaaccaat gtgtaccatc      360
18      caggagttat tctatgacaa aacaaaaagt tttgttcttg tgtacttctc tgtgcaccat      420
19      ctttctatat ctatttagaa aacaaaacaa attttggtaa cacgcttggtg tataaagagc      480
20      aggacagcgg tgtcacagat caacctagaa agtaattatt taacgagtaa atgactcata      540
21      taggacaagg caagctgtga ctttcaacct gttctgtctc gtgccgaatt cggcacgagc      600
22      caaagcctac ctggacccta ccacc atg tca gga tcc aca cag cct gtg gca      652
23                      Met Ser Gly Ser Thr Gln Pro Val Ala
24                      1                      5
25      cag aca tgg cgg gct gct gag ccc cgc tac cca ccc cat ggc atc tcc      700
26      Gln Thr Trp Arg Ala Ala Glu Pro Arg Tyr Pro Pro His Gly Ile Ser
27      10                      15                      20                      25
28      tac ccg gtg cag ata gcc cgg tcc cac acg gac gtg ggg ctg ctt gag      748
29      Tyr Pro Val Gln Ile Ala Arg Ser His Thr Asp Val Gly Leu Leu Glu
30                      30                      35                      40
31      tac caa cac cac ccc cgt gac tac acc tca cac ctg tca ccc ggt tcc      796
32      Tyr Gln His His Pro Arg Asp Tyr Thr Ser His Leu Ser Pro Gly Ser
33                      45                      50                      55
34      atc atc cag cca cag agg agg cgg ccc tca ctg ctg tca gag ttc cag      844
35      Ile Ile Gln Pro Gln Arg Arg Arg Pro Ser Leu Leu Ser Glu Phe Gln
36                      60                      65                      70
37      cct ggg agt gaa cgg tct cag gag ctc cac ctg cgc cct gag tcc cgc      892
38      Pro Gly Ser Glu Arg Ser Gln Glu Leu His Leu Arg Pro Glu Ser Arg
39                      75                      80                      85
40      acg ttc ctg cct gag ctg ggc aag ccc gac ata gaa ttc acc gag agc      940
41      Thr Phe Leu Pro Glu Leu Gly Lys Pro Asp Ile Glu Phe Thr Glu Ser
42                      90                      95                      100                      105
43      aag cgc ccc cgc ctg gag cta cta ccc gat acc ctg ctg cgc cca tca      988
44      Lys Arg Pro Arg Leu Glu Leu Leu Pro Asp Thr Leu Leu Arg Pro Ser
45                      110                      115                      120
46      ccc ctg ctg gcc act ggg cag ccg agt ggg tct gaa gac ctt acc aag      1036
47      Pro Leu Leu Ala Thr Gly Gln Pro Ser Gly Ser Glu Asp Leu Thr Lys

```



48

49

50

115

130

gac cgt agc ctg gca ggc aag ctg gag cct gtg tca cct ccc agt ccc  
Asp Arg Ser Leu Ala Gly Lys Leu Glu Pro Val Ser Pro Pro Ser Pro

1084

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/09/522,753**

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51		140		145		150			
52	ccg	cac	gct	gac	cct	gag	cta	gag	ctg
53	Pro	His	Ala	Asp	Pro	Glu	Leu	Glu	Leu
54		155		160		165			
55	gag	gag	ctg	atc	cag	aac	atg	gac	cgc
56	Glu	Glu	Leu	Ile	Gln	Asn	Met	Asp	Arg
57		170		175		180		185	
58	gta	gag	cag	cag	atc	tcc	aag	ctg	aag
59	Val	Glu	Gln	Gln	Ile	Ser	Lys	Leu	Lys
60				190		195		200	
61	gag	gag	gcc	gcc	aag	ccg	ccc	gaa	ccc
62	Glu	Glu	Ala	Ala	Lys	Pro	Pro	Glu	Pro
63			205			210		215	
64	ccc	ata	gaa	tca	aag	cac	cga	agc	ctg
65	Pro	Ile	Glu	Ser	Lys	His	Arg	Ser	Leu
66		220		225		230			
67	aac	cgg	aag	aaa	gcc	gaa	gcc	gca	cac
68	Asn	Arg	Lys	Lys	Ala	Glu	Ala	Ala	His
69		235		240		245			
70	ccc	cag	gtg	gag	ctg	cct	ctg	tac	aac
71	Pro	Gln	Val	Glu	Leu	Pro	Leu	Tyr	Asn
72		250		255		260		265	
73	tac	cat	gaa	aac	atc	aaa	ata	aac	cag
74	Tyr	His	Glu	Asn	Ile	Lys	Ile	Asn	Gln
75			270		275		280		
76	ttg	tac	ttt	aag	cgg	agg	aac	cac	gcg
77	Leu	Tyr	Phe	Lys	Arg	Arg	Asn	His	Ala
78		285		290		295			
79	ttc	tgc	cag	cgc	tat	gac	cag	ctc	atg
80	Phe	Cys	Gln	Arg	Tyr	Asp	Gln	Leu	Met
81		300		305		310			
82	gag	cgc	ata	gag	aac	aat	ccg	cga	agg
83	Glu	Arg	Ile	Glu	Asn	Asn	Pro	Arg	Arg
84		315		320		325			
85	agg	gag	tac	tac	gag	aaa	cag	ttc	ccg
86	Arg	Glu	Tyr	Tyr	Glu	Lys	Gln	Phe	Pro
87		330		335		340		345	
88	ctg	cag	gag	cgc	atg	cag	agc	agg	gtg
89	Leu	Gln	Glu	Arg	Met	Gln	Ser	Arg	Val
90			350		355		360		
91	tcc	atg	tcg	gct	gcc	cgc	agt	gag	cat
92	Ser	Met	Ser	Ala	Ala	Arg	Ser	Glu	His
93		365		370		375			
94	ggc	ttg	tct	gag	cag	gag	aac	ctg	gag
95	Gly	Leu	Ser	Glu	Gln	Glu	Asn	Leu	Glu
96		380		385		390			
97	gtg	atc	ccg	ccc	atg	ttg	tac	gac	gcg
98	Val	Ile	Pro	Pro	Met	Leu	Tyr	Asp	Ala
99		395		400		405			
100	atc	aac	atg	aat	gga	ctc	atg	gat	gac

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/522,753

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101	Ile Asn Met Asn Gly Leu Met Asp Asp Pro Met Lys Val Tyr Lys Asp	
102	410 415 420 425	
103	cgt cag gtt acc aac atg tgg agc gag cag gag agg gac acc ttc cgt	1948
104	Arg Gln Val Thr Asn Met Trp Ser Glu Gln Glu Arg Asp Thr Phe Arg	
105	430 435 440	
106	gag aag ttt atg cag cac cct aag aac ttt ggc ctg att gcc tca ttc	1996
107	Glu Lys Phe Met Gln His Pro Lys Asn Phe Gly Leu Ile Ala Ser Phe	
108	445 450 455	
109	ctg gag aga aag acg gtc gct gag tgt gtc ctc tat tac tac ctg acc	2044
110	Leu Glu Arg Lys Thr Val Ala Glu Cys Val Leu Tyr Tyr Tyr Leu Thr	
111	460 465 470	
112	aag aag aat gaa aat tac aag agc ttg gtg agg cgg agc tat cgg cgc	2092
113	Lys Lys Asn Glu Asn Tyr Lys Ser Leu Val Arg Arg Ser Tyr Arg Arg	
114	475 480 485	
115	cgt ggc aag agc cag cag cag cag cag cag caa caa cag cag cag cag	2140
116	Arg Gly Lys Ser Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	
117	490 495 500 505	
118	cag cag atg gca cgg agc agc cag gag gag aag gag gag aag gag aag	2188
119	Gln Gln Met Ala Arg Ser Ser Gln Glu Glu Lys Glu Glu Lys Glu Lys	
120	510 515 520	
121	gag aag gag gcc gac aag gag gaa gag aag cag gat gcg gag aac gag	2236
122	Glu Lys Glu Ala Asp Lys Glu Glu Glu Lys Gln Asp Ala Glu Asn Glu	
123	525 530 535	
124	aag gaa gaa ctc agc aag gag aag aca gac gac act tct ggc gag gac	2284
125	Lys Glu Glu Leu Ser Lys Glu Lys Thr Asp Asp Thr Ser Gly Glu Asp	
126	540 545 550	
127	aac cat gag aaa gag gcc gtg gcc tcc aaa ggc cgc aaa act gcc aac	2332
128	Asn His Glu Lys Glu Ala Val Ala Ser Lys Gly Arg Lys Thr Ala Asn	
129	555 560 565	
130	agc caa ggc cgc cgc aaa ggc cgt atc acg cgc tcc atg gcc aac gag	2380
131	Ser Gln Gly Arg Arg Lys Gly Arg Ile Thr Arg Ser Met Ala Asn Glu	
132	570 575 580 585	
133	gcc aac cat gag gag aca gcc acc cca cag caa agt tca gag ctg gct	2428
134	Ala Asn His Glu Glu Thr Ala Thr Pro Gln Gln Ser Ser Glu Leu Ala	
135	590 595 600	
136	tcc atg gag atg aac gag agt tct cgc tgg act gag gaa gag atg gag	2476
137	Ser Met Glu Met Asn Glu Ser Ser Arg Trp Thr Glu Glu Glu Met Glu	
138	605 610 615	
139	aca gca aag aaa ggc ctc ctg gaa cat ggg agg aac tgg tca gcc att	2524
140	Thr Ala Lys Lys Gly Leu Leu Glu His Gly Arg Asn Trp Ser Ala Ile	
141	620 625 630	
142	gcc cgc atg gtg ggc tcc aag acc gtg tcc cag tgt aag aac ttc tac	2572
143	Ala Arg Met Val Gly Ser Lys Thr Val Ser Gln Cys Lys Asn Phe Tyr	
144	635 640 645	
145	ttc aac tac aag aag agg cag aac ctg gac gaa atc ctt cag cag cac	2620
146	Phe Asn Tyr Lys Lys Arg Gln Asn Leu Asp Glu Ile Leu Gln Gln His	
147	650 655 660 665	
148	aag cta aag atg gag aag gag agg aac gct cgg agg aag aag aag aag	2668
149	Lys Leu Lys Met Glu Lys Glu Arg Asn Ala Arg Arg Lys Lys Lys Lys	
150	670 675 680	

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151	acc cca gct gcg gcg agc gag gag aca gcc ttc cca cct gcc gct gag	2716
152	Thr Pro Ala Ala Ala Ser Glu Glu Thr Ala Phe Pro Pro Ala Ala Glu	
153	685 690 695	
154	gac gaa gag atg gaa gca tca ggc gca agt gcc aat gag gaa gag ctg	2764
155	Asp Glu Glu Met Glu Ala Ser Gly Ala Ser Ala Asn Glu Glu Glu Leu	
156	700 705 710	
157	gcg gag gag gca gaa gcc tca cag gcc tct ggg aat gag gtt ccc aga	2812
158	Ala Glu Glu Ala Glu Ala Ser Gln Ala Ser Gly Asn Glu Val Pro Arg	
159	715 720 725	
160	gtt ggg gag tgc agt ggc cca gct gct gtc aac aac agc tct gat act	2860
161	Val Gly Glu Cys Ser Gly Pro Ala Ala Val Asn Asn Ser Ser Asp Thr	
162	730 735 740 745	
163	gag agt gtc cca tcc ccg cgt tca gaa gcc atg aag gac act ggg cct	2908
164	Glu Ser Val Pro Ser Pro Arg Ser Glu Ala Met Lys Asp Thr Gly Pro	
165	750 755 760	
166	aaa ccc act ggc act gaa gca ttg ccc gct gcc acc cag cca cct gtt	2956
167	Lys Pro Thr Gly Thr Glu Ala Leu Pro Ala Ala Thr Gln Pro Pro Val	
168	765 770 775	
169	cct cct cca gaa gaa ccg gca gta gcc cct gct gag ccc tcc cca gtc	3004
170	Pro Pro Pro Glu Glu Pro Ala Val Ala Pro Ala Glu Pro Ser Pro Val	
171	780 785 790	
172	cct gat gcc agt ggc cca cca tcc cca gag cct tcc cat cac ctg ccg	3052
173	Pro Asp Ala Ser Gly Pro Pro Ser Pro Glu Pro Ser His His Leu Pro	
174	795 800 805	
175	cac ccc cgg cta ctg tgg aca agg atg aac aag aag ccc cgg ctg ctc	3100
176	His Pro Arg Leu Leu Trp Thr Arg Met Asn Lys Lys Pro Arg Leu Leu	
177	810 815 820 825	
178	cag ctc ccc aga cag agg atg cca agg agc aga agt ctg agg ccg agg	3148
179	Gln Leu Pro Arg Gln Arg Met Pro Arg Ser Arg Ser Leu Arg Pro Arg	
180	830 835 840	
181	aga tcg atg tgg gaa aag cca gag gag ccc gag gcc tct gag gag ccc	3196
182	Arg Ser Met Trp Glu Lys Pro Glu Glu Pro Glu Ala Ser Glu Glu Pro	
183	845 850 855	
184	ccg gag agt gta aag agt gac cac aag gag gag acc gag gaa gag cct	3244
185	Pro Glu Ser Val Lys Ser Asp His Lys Glu Glu Thr Glu Glu Glu Pro	
186	860 865 870	
187	gaa gac aaa gcc aag ggc aca gag gcc att gaa act gtg tct gag gca	3292
188	Glu Asp Lys Ala Lys Gly Thr Glu Ala Ile Glu Thr Val Ser Glu Ala	
189	875 880 885	
190	cca ctt aag gtg gag gag gct ggt agc aag gca gct gtg acc aag ggt	3340
191	Pro Leu Lys Val Glu Glu Ala Gly Ser Lys Ala Ala Val Thr Lys Gly	
192	890 895 900 905	
193	tcc agc tca ggt gcc acc cag gac agt gac ttc agt gcc acc tgc agt	3388
194	Ser Ser Ser Gly Ala Thr Gln Asp Ser Asp Phe Ser Ala Thr Cys Ser	
195	910 915 920	
196	gcc gat gag gtg gac gaa ccc gaa gga ggt gac aag ggc agg ctg ctg	3436
197	Ala Asp Glu Val Asp Glu Pro Glu Gly Gly Asp Lys Gly Arg Leu Leu	
198	925 930 935	
199	tca cca agg ccc agc ctc ctc acc ccg gct gga gat ccc cgg gcc agt	3484
200	Ser Pro Arg Pro Ser Leu Leu Thr Pro Ala Gly Asp Pro Arg Ala Ser	

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201		940		945		950		
202	acc	tcg	ccc	cag	aag	ccg	ctg	gac
203	Thr	Ser	Pro	Gln	Lys	Pro	Leu	Asp
204		955		960		965		
205	gcc	gcc	atc	ccc	cct	atc	cag	gtc
206	Ala	Ala	Ile	Pro	Pro	Ile	Gln	Val
207		970		975		980		985
208	gag	gac	aca	gta	ccc	cca	aag	cca
209	Glu	Asp	Thr	Val	Pro	Pro	Lys	Pro
210			990			995		1000
211	cag	cac	cta	cag	cca	gag	ggt	gac
212	Gln	His	Leu	Gln	Pro	Glu	Gly	Asp
213			1005			1010		1015
214	cca	cgt	ggc	aag	tcc	cgc	agc	cca
215	Pro	Arg	Gly	Lys	Ser	Arg	Ser	Pro
216			1020			1025		1030
217	gag	aaa	ccc	gca	ttc	ttt	ccg	gct
218	Glu	Lys	Pro	Ala	Phe	Phe	Pro	Ala
219			1035			1040		1045
220	ccg	act	gag	ccc	cca	cgc	tgg	tca
221	Pro	Thr	Glu	Pro	Pro	Arg	Trp	Ser
222			1050			1055		1060
223	cca	cgg	gag	gtg	atc	aag	act	tcc
224	Pro	Arg	Glu	Val	Ile	Lys	Thr	Ser
225				1070			1075	1080
226	ttc	tcc	tac	aca	ccc	ccc	ggt	cac
227	Phe	Ser	Tyr	Thr	Pro	Pro	Gly	His
228			1085			1090		1095
229	agt	gcc	cgg	ccc	gtc	ctg	cca	cgt
230	Ser	Ala	Arg	Pro	Val	Leu	Pro	Arg
231			1100			1105		1110
232	ctc	atc	tcc	tct	gcc	aag	cat	ccc
233	Leu	Ile	Ser	Ser	Ala	Lys	His	Pro
234			1115			1120		1125
235	gcc	atc	tcc	cag	cag	ggg	atg	tca
236	Ala	Ile	Ser	Gln	Gln	Gly	Met	Ser
237			1130			1135		1140
238	gag	cat	gcc	aag	gcc	ccc	atg	ggc
239	Glu	His	Ala	Lys	Ala	Pro	Met	Gly
240				1150			1155	1160
241	gcc	gtg	gac	cct	aag	aag	ctg	ggg
242	Ala	Val	Asp	Pro	Lys	Lys	Leu	Gly
243			1165			1170		1175
244	gga	agc	atc	acc	aag	ggc	ctc	ccc
245	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Pro
246			1180			1185		1190
247	agc	tac	aga	ggc	tct	atc	acc	cac
248	Ser	Tyr	Arg	Gly	Ser	Ile	Thr	His
249			1195			1200		1205
250	aag	ggt	acc	atc	agc	agg	atc	gtc

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251	Lys Gly Thr Ile Ser Arg Ile Val Gly Glu Asp Ser Pro Ser Arg Leu	
252	1210 1215 1220 1225	
253	gac cgg gca cga gag gac acc ctg ccc aag ggc cat gtc atc tat gag	4348
254	Asp Arg Ala Arg Glu Asp Thr Leu Pro Lys Gly His Val Ile Tyr Glu	
255	1230 1235 1240	
256	ggc aag aaa ggc cac gtc cta tcc tat gaa ggt ggt atg tcc gtg tca	4396
257	Gly Lys Lys Gly His Val Leu Ser Tyr Glu Gly Gly Met Ser Val Ser	
258	1245 1250 1255	
259	cag tgc tct aag gag gat gga agg agc agc tcg ggc cca ccc cat gag	4444
260	Gln Cys Ser Lys Glu Asp Gly Arg Ser Ser Ser Gly Pro Pro His Glu	
261	1260 1265 1270	
262	act gcc gcc cct aaa cgc acc tat gac atg atg gag ggc cgt gta ggc	4492
263	Thr Ala Ala Pro Lys Arg Thr Tyr Asp Met Met Glu Gly Arg Val Gly	
264	1275 1280 1285	
265	agg act gtc acc tca gcc agc ata gag gga ctc atg ggc cgc gcc atc	4540
266	Arg Thr Val Thr Ser Ala Ser Ile Glu Gly Leu Met Gly Arg Ala Ile	
267	1290 1295 1300 1305	
268	cct gag cag cac agc ccc cac ctc aag gag cag cat cac atc cga ggc	4588
269	Pro Glu Gln His Ser Pro His Leu Lys Glu Gln His His Ile Arg Gly	
270	1310 1315 1320	
271	tcc atc acg caa ggc atc ccg agg tcc tat gtg gag gcg cag gag gac	4636
272	Ser Ile Thr Gln Gly Ile Pro Arg Ser Tyr Val Glu Ala Gln Glu Asp	
273	1325 1330 1335	
274	tac tta cgg cgg gag gcc aag ctc ttg aag cga gaa ggg aca cca cca	4684
275	Tyr Leu Arg Arg Glu Ala Lys Leu Leu Lys Arg Glu Gly Thr Pro Pro	
276	1340 1345 1350	
277	ccc cca cca cca cct cgg gac ctg act gag acc tac aag ccc cgg ccc	4732
278	Pro Pro Pro Pro Pro Arg Asp Leu Thr Glu Thr Tyr Lys Pro Arg Pro	
279	1355 1360 1365	
280	ctg gac cct ctg ggt ccc ctg aag ctg aag ccg act cac gag ggt gtg	4780
281	Leu Asp Pro Leu Gly Pro Leu Lys Leu Lys Pro Thr His Glu Gly Val	
282	1370 1375 1380 1385	
283	gta gca act gtg aag gag gcg ggc cgc tct atc cat gag atc ccg aga	4828
284	Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile Pro Arg	
285	1390 1395 1400	
286	gag gag ctg cgc cgc aca cct gag cta ccc ctg gca cca cgg cct ctg	4876
287	Glu Glu Leu Arg Arg Thr Pro Glu Leu Pro Leu Ala Pro Arg Pro Leu	
288	1405 1410 1415	
289	aag gag ggt tcc atc acc cag ggc acc cca ctc aag tac gac tct ggg	4924
290	Lys Glu Gly Ser Ile Thr Gln Gly Thr Pro Leu Lys Tyr Asp Ser Gly	
291	1420 1425 1430	
292	gca ccc tcc act ggc acc aag aaa cac gac gtg cgc tcc atc atc ggc	4972
293	Ala Pro Ser Thr Gly Thr Lys Lys His Asp Val Arg Ser Ile Ile Gly	
294	1435 1440 1445	
295	agc ccc ggc cgg cct ttc cct gcc ctg cac ccg ctg gac ata atg gct	5020
296	Ser Pro Gly Arg Pro Phe Pro Ala Leu His Pro Leu Asp Ile Met Ala	
297	1450 1455 1460 1465	
298	gac gcc cgg gca ctg gag cgt gcc tgc tat gaa gag agt ctg aag agc	5068
299	Asp Ala Arg Ala Leu Glu Arg Ala Cys Tyr Glu Glu Ser Leu Lys Ser	
300	1470 1475 1480	

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301	cgg tca ggg acc agc agt ggt gca ggg ggc tcc atc aca cgt ggg gct	5116
302	Arg Ser Gly Thr Ser Ser Gly Ala Gly Gly Ser Ile Thr Arg Gly Ala	
303	1485 1490 1495	
304	cca gtc gtc gtg cct gaa ctg ggc aag cca cgg caa agc cca ctg act	5164
305	Pro Val Val Val Pro Glu Leu Gly Lys Pro Arg Gln Ser Pro Leu Thr	
306	1500 1505 1510	
307	tac gaa gac cac ggg gca ccc ttc acc agt cac ctg cca cgt ggc tcc	5212
308	Tyr Glu Asp His Gly Ala Pro Phe Thr Ser His Leu Pro Arg Gly Ser	
309	1515 1520 1525	
310	cct gtg acc acg agg gag ccc acg cca cgc ctt cag gaa ggc agc ctc	5260
311	Pro Val Thr Thr Arg Glu Pro Thr Pro Arg Leu Gln Glu Gly Ser Leu	
312	1530 1535 1540 1545	
313	cta tcc agc aag gcg tcc cag gac cgg aag ctg aca tct aca ccc cgg	5308
314	Leu Ser Ser Lys Ala Ser Gln Asp Arg Lys Leu Thr Ser Thr Pro Arg	
315	1550 1555 1560	
316	gag atc gcc aag tcc cca cac agc act gtg ccc gag cac cac cct cac	5356
317	Glu Ile Ala Lys Ser Pro His Ser Thr Val Pro Glu His His Pro His	
318	1565 1570 1575	
319	ccc atc tcc ccc tat gag cac ttg ctc cgg ggc gtg act ggt gtg gac	5404
320	Pro Ile Ser Pro Tyr Glu His Leu Leu Arg Gly Val Thr Gly Val Asp	
321	1580 1585 1590	
322	ctg tac cgt ggt cac atc cca ttg gcc ttt gac ccc acc tcc ata ccc	5452
323	Leu Tyr Arg Gly His Ile Pro Leu Ala Phe Asp Pro Thr Ser Ile Pro	
324	1595 1600 1605	
325	cga ggg atc cct ctg gaa gca gca gcc gca gcc tac tac ctg ccc cgg	5500
326	Arg Gly Ile Pro Leu Glu Ala Ala Ala Ala Tyr Tyr Leu Pro Arg	
327	1610 1615 1620 1625	
328	cac ttg gcc ccc agc ccc acc tac cca cac ctg tac cca cct tac ctc	5548
329	His Leu Ala Pro Ser Pro Thr Tyr Pro His Leu Tyr Pro Pro Tyr Leu	
330	1630 1635 1640	
331	atc cgc ggc tac cct gac acg gcg gcc ctg gag aac cgc cag acc atc	5596
332	Ile Arg Gly Tyr Pro Asp Thr Ala Ala Leu Glu Asn Arg Gln Thr Ile	
333	1645 1650 1655	
334	atc aat gac tac atc acc tcg cag cag atg cac cac aac gct gcc tcc	5644
335	Ile Asn Asp Tyr Ile Thr Ser Gln Gln Met His His Asn Ala Ala Ser	
336	1660 1665 1670	
337	gcc atg gcc cag cgt gct gac atg ctg agg ggt ctg tca ccg cga gag	5692
338	Ala Met Ala Gln Arg Ala Asp Met Leu Arg Gly Leu Ser Pro Arg Glu	
339	1675 1680 1685	
340	tcc tcg ctg gcc ctc aat tat gcc gct ggc cca aga ggc att atc gac	5740
341	Ser Ser Leu Ala Leu Asn Tyr Ala Ala Gly Pro Arg Gly Ile Ile Asp	
342	1690 1695 1700 1705	
343	ctg tcc caa gtg cca cac ctg ccc gtg ctg gtg cca cca acg cca ggc	5788
344	Leu Ser Gln Val Pro His Leu Pro Val Leu Val Pro Pro Thr Pro Gly	
345	1710 1715 1720	
346	acc cct gcc acc gcc atc gac cgc ctt gcc tac ctc ccc act gcg ccc	5836
347	Thr Pro Ala Thr Ala Ile Asp Arg Leu Ala Tyr Leu Pro Thr Ala Pro	
348	1725 1730 1735	
349	cca ccc ttc agc agc cgc cac agt agc tca ccg ctg tcc cca gga ggc	5884
350	Pro Pro Phe Ser Ser Arg His Ser Ser Ser Pro Leu Ser Pro Gly Gly	

[illegible]



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401	Glu Pro Ile Ser Pro Val Ser Ser Pro Ser Leu Thr His Asp Lys Gly	
402	2010 2015 2020 2025	
403	ctc tcc aaa cct ctg gaa gag cta gag aag agc cac ttg gaa ggg gag	6748
404	Leu Ser Lys Pro Leu Glu Glu Leu Glu Lys Ser His Leu Glu Gly Glu	
405	2030 2035 2040	
406	ctg cgg cac aag cag cca ggc ccc atg aag ctc agc gcg gag gct gcc	6796
407	Leu Arg His Lys Gln Pro Gly Pro Met Lys Leu Ser Ala Glu Ala Ala	
408	2045 2050 2055	
409	cat ctc cca cat ctg cgg cca ctg ccc gag agc cag ccc tca tcc agc	6844
410	His Leu Pro His Leu Arg Pro Leu Pro Glu Ser Gln Pro Ser Ser Ser	
411	2060 2065 2070	
412	cca ctc ctc cag act gcc cca ggc atc aaa ggt cac cag agg gtg gtc	6892
413	Pro Leu Leu Gln Thr Ala Pro Gly Ile Lys Gly His Gln Arg Val Val	
414	2075 2080 2085	
415	acc ctg gct cag cac atc agc gag gtc att acg cag gac tac acg cgc	6940
416	Thr Leu Ala Gln His Ile Ser Glu Val Ile Thr Gln Asp Tyr Thr Arg	
417	2090 2095 2100 2105	
418	cac cac ccg cag cag ctc agt ggc ccc ctt ccc gcc cct ctc tac tcc	6988
419	His His Pro Gln Gln Leu Ser Gly Pro Leu Pro Ala Pro Leu Tyr Ser	
420	2110 2115 2120	
421	ttt ccc gga gcc agc tgc cct gtc ctg gat ctt cgc cgc cca ccc agt	7036
422	Phe Pro Gly Ala Ser Cys Pro Val Leu Asp Leu Arg Arg Pro Pro Ser	
423	2125 2130 2135	
424	gac ctc tac ctc cca ccc ccc gac cat ggc acc cca gcc cgg gga tcc	7084
425	Asp Leu Tyr Leu Pro Pro Pro Asp His Gly Thr Pro Ala Arg Gly Ser	
426	2140 2145 2150	
427	ccc cac agt gaa ggg ggc aaa agg tcc cca gaa ccc agc aaa aca tcg	7132
428	Pro His Ser Glu Gly Gly Lys Arg Ser Pro Glu Pro Ser Lys Thr Ser	
429	2155 2160 2165	
430	gtc ctg ggc agc agc gag gat gcc att gag cct gtg tcc cca cca gag	7180
431	Val Leu Gly Ser Ser Glu Asp Ala Ile Glu Pro Val Ser Pro Pro Glu	
432	2170 2175 2180 2185	
433	ggc atg act gag cca gga cat gct cgg agc act gcg tac cca ctg ctg	7228
434	Gly Met Thr Glu Pro Gly His Ala Arg Ser Thr Ala Tyr Pro Leu Leu	
435	2190 2195 2200	
436	tat cga gac ggg gaa cag ggc gag ccc agg atg ggt cta gag tct cca	7276
437	Tyr Arg Asp Gly Glu Gln Gly Glu Pro Arg Met Gly Leu Glu Ser Pro	
438	2205 2210 2215	
439	ggc aac acc agc cag ccg cca acc ttc ttc agt aag ctg act gag agc	7324
440	Gly Asn Thr Ser Gln Pro Pro Thr Phe Phe Ser Lys Leu Thr Glu Ser	
441	2220 2225 2230	
442	aac tcc gcc atg gtg aag tcg aag aag cag gag atc aac aag aaa ctc	7372
443	Asn Ser Ala Met Val Lys Ser Lys Lys Gln Glu Ile Asn Lys Lys Leu	
444	2235 2240 2245	
445	aac acc cac aac cgg aac gag cca gaa tac aat att ggc cag cct ggg	7420
446	Asn Thr His Asn Arg Asn Glu Pro Glu Tyr Asn Ile Gly Gln Pro Gly	
447	2250 2255 2260 2265	
448	acg gaa atc ttc aac atg ccc gcc atc act gga gca ggc ctt atg acc	7468
449	Thr Glu Ile Phe Asn Met Pro Ala Ile Thr Gly Ala Gly Leu Met Thr	
450	2270 2275 2280	

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451	tgt aga agc cag gcg gtg caa gaa cac gcc agc acc aac atg ggg cta	7516
452	Cys Arg Ser Gln Ala Val Gln Glu His Ala Ser Thr Asn Met Gly Leu	
453	2285 2290 2295	
454	gag gcc att att aga aag gca ctc atg ggt aaa tat gat cag tgg gaa	7564
455	Glu Ala Ile Ile Arg Lys Ala Leu Met Gly Lys Tyr Asp Gln Trp Glu	
456	2300 2305 2310	
457	gag ccc ccg ccg ctc ggc gcc aat gct ttt aac cct ctg aat gcc agc	7612
458	Glu Pro Pro Pro Leu Gly Ala Asn Ala Phe Asn Pro Leu Asn Ala Ser	
459	2315 2320 2325	
460	gcc agt ctg ccc gct gct gct atg ccc ata acc act gct gac gga cgg	7660
461	Ala Ser Leu Pro Ala Ala Ala Met Pro Ile Thr Thr Ala Asp Gly Arg	
462	2330 2335 2340 2345	
463	agt gac cac gca ctc acc tcg cca ggt gga ggt ggg aaa gcc aag gtc	7708
464	Ser Asp His Ala Leu Thr Ser Pro Gly Gly Gly Gly Lys Ala Lys Val	
465	2350 2355 2360	
466	tct ggc aga cct agc agc cga aaa gcc aag tcg cca gca cca ggc cta	7756
467	Ser Gly Arg Pro Ser Ser Arg Lys Ala Lys Ser Pro Ala Pro Gly Leu	
468	2365 2370 2375	
469	gcg tcc gga gac cga ccc cct tct gtc tcc tca gta cac tca gag ggg	7804
470	Ala Ser Gly Asp Arg Pro Pro Ser Val Ser Ser Val His Ser Glu Gly	
471	2380 2385 2390	
472	gac tgc aat cgc cga aca cca ctc acc aac cgt gtg tgg gag gac cgg	7852
473	Asp Cys Asn Arg Arg Thr Pro Leu Thr Asn Arg Val Trp Glu Asp Arg	
474	2395 2400 2405	
475	ccc tca tct gca ggg tcc acg cca ttc ccc tac aac cct ttg att atg	7900
476	Pro Ser Ser Ala Gly Ser Thr Pro Phe Pro Tyr Asn Pro Leu Ile Met	
477	2410 2415 2420 2425	
478	agg cta cag gca ggt gtc atg gcc tcc ccg ccc cca cct ggc ctt gcg	7948
479	Arg Leu Gln Ala Gly Val Met Ala Ser Pro Pro Pro Pro Gly Leu Ala	
480	2430 2435 2440	
481	gca ggc agc ggg ccc cta gct ggt ccc cac cac gcc tgg gat gag gag	7996
482	Ala Gly Ser Gly Pro Leu Ala Gly Pro His His Ala Trp Asp Glu Glu	
483	2445 2450 2455	
484	ccc aag cca ctg ctg tgt tca cag tat gag aca ctc tcg gac agc gag	8044
485	Pro Lys Pro Leu Leu Cys Ser Gln Tyr Glu Thr Leu Ser Asp Ser Glu	
486	2460 2465 2470	
487	tga ccacggattg ggggggagcg gtgccaggtc ccgcacaagg cagaagcagc	8097
488	ccagcatgga gcagacagct gctgactccc gagactgagg aaggagcccc tgagtctgcc	8157
489	tgcgcggtcca tccgtncgtc gtncactcat ctgtccatcc agagctggca ttctgcctgt	8217
490	ctaaagcctt aactaagact tccaccccg gctggccctg cgcagtgacc ttacactcag	8277
491	gggattgttt accttggtgc tcganaagg gtagtgagaca ggaaggggag ggacaagccg	8337
492	ggccangagg gggggggaca ancaattcgt gtgtcaagtc gcactcntgc t	8388